The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A hGT1 gene containing transcribed polymorphic CAG repeat, which comprises a sequence as set forth in Fig. 3 and Figs. 4A-4C, wherein allelic variants of CAG repeat are selected from the group consisting of alleles -3, -2, -1, 0 and 1, and wherein said allelic variants are associated with schizophrenia, affective disorders, neurodevelopmental brain diseases or with phenotypic variability with respect to long term response to neuroleptic medication.

2. The gene of claim 1, wherein said affective disorder is manic depression.

3. A method for the prognosis of severity of schizophrenia of a patient, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of CAG repeat of the gene of claim 1, and wherein allelic variants shorter than allele 0 are indicative of non-severe schizophrenia.

4. A method for the identification of patient responding to neuroleptic medication, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of CAG repeat of the gene of claim 1, and wherein allelic

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variants shorter than allele 0 are indicative of neuroleptic response.

5. The method of claim 4, wherein said shorter allelic variants have from about 171 to about 177 bp in length.

6. A non-human mammal model for the hGT1 gene of claim 1, whose germ cells and somatic cells are transformed and expresses at least one allelic variant of the hGT1 gene and wherein said allelic variant of the hGT1 being introduced into the mammal, or an ancestor of the mammal, at an embryonic stage.

7. A method for the screening of therapeutic agents for the prevention and/or treatment of schizophrenia, which comprises the steps of:

a) administering said therapeutic agents to the non-human mammal of claim 6 or schizophrenia patients; and

b) evaluating the prevention and/or treatment of development of schizophrenia in said mammal or said patients.

8. A method to identify genes part of or interacting with a biochemical pathway affected by hGT1 gene which comprises the steps of:

a) designing probes and/or primers using the hGT1 gene of claim 1 and screening psychiatric patients samples with said probes and/or primers; and

b) evaluating the identified gene role in psychiatric patients.

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9. A method of categorizing psychiatric patients according to their genotype to maximize response to treatment patients, which comprises the steps of:

a) obtaining a nucleic acid sample of said patients; and

b) determining allelic variants of CAG repeat of the gene of claim 1, wherein patients are categorized with respect to their allelic variants and wherein allelic variants shorter than allele 0 are indicative of neuroleptic response.

10. The use of the determination of allelic variants of CAG repeat of the gene of claim 1 for the identification of patient responding to neuroleptic medication, wherein allelic variants shorter than allele 0 are indicative of neuroleptic response.

11. The use of claim 10, wherein said shorter allelic variants have from about 171 to about 177 bp in length.

12. The use of the model of claim 6 for the screening of therapeutic agents for the manufacture of a medicament for prevention and/or treatment of schizophrenia.